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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 23:35:56 ; Search time 45.5 Seconds
(without alignments)
10278.727 Million cell updates/sec

Title: US-10-025-514-15

Perfect score: 1525

Sequence: 1 tctagaccatgaagaccct.....ccagtcaggcctagtcgac 1525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629.4	41.3	1308	3	US-09-023-173-10
2	629.4	41.3	1308	3	US-09-023-339-6
3	628.4	41.2	1185	3	US-09-023-339-3
4	628.4	41.2	1260	3	US-09-023-173-5
5	429	28.1	1185	3	US-09-023-339-2
6	429	28.1	5932	4	US-09-299-141-4
7	429	28.1	6142	4	US-09-299-141-8
8	429	28.1	6565	4	US-09-299-141-1
9	429	28.1	6714	4	US-09-299-141-6
10	429	28.1	6924	4	US-09-299-141-9
11	429	28.1	6924	4	US-09-299-141-10
12	429	28.1	6981	4	US-09-299-141-11
13	429	28.1	7054	4	US-09-299-141-7
14	429	28.1	7405	4	US-09-299-141-3
15	429	28.1	7405	4	US-09-299-141-2
16	404.6	26.5	1356	1	US-08-002-202-16
17	404.6	26.5	1356	3	US-08-481-534-16
18	403	26.4	1356	1	US-08-002-202-12
19	403	26.4	1356	3	US-08-481-534-12
20	399.8	26.2	1356	1	US-08-002-202-18
21	399.8	26.2	1356	3	US-08-481-534-18
22	311.8	20.4	1339	1	US-07-859-480-1
23	227.2	14.9	7492	4	US-09-299-141-5
24	219.8	14.4	1423	1	US-07-829-954-1
25	219.8	14.4	1423	1	US-07-994-423-1
26	219.8	14.4	1423	1	US-08-421-891-1
27	207.8	13.6	10627	1	US-08-060-925A-12

28	125.4	8.2	194	4	US-07-963-538B-5	Sequence 5, Appl
29	124.6	8.2	2466	4	US-09-271-608-7	Sequence 7, Appl
30	124.6	8.2	2466	4	US-09-695-980-7	Sequence 7, Appl
31	124.6	8.2	2466	4	US-09-696-147-7	Sequence 7, Appl
32	124.6	8.2	2466	4	US-09-696-364-7	Sequence 7, Appl
33	123	8.1	180	3	US-08-483-503A-2	Sequence 2, Appl
34	106.4	7.0	1508	3	US-08-660-347-1	Sequence 1, Appl
35	81.6	5.4	1179	4	US-08-745-995A-22	Sequence 22, Appl
36	81.6	5.4	1179	4	US-08-745-995A-23	Sequence 23, Appl
37	81.6	5.4	1191	4	US-08-745-985A-4	Sequence 4, Appl
38	81.6	5.4	1191	4	US-08-745-995A-5	Sequence 5, Appl
39	81.6	5.4	1191	4	US-08-745-995A-34	Sequence 34, Appl
40	81.6	5.4	1191	4	US-08-745-995A-35	Sequence 35, Appl
41	81.6	5.4	1197	4	US-08-745-995A-10	Sequence 10, Appl
42	81.6	5.4	1197	4	US-08-745-995A-11	Sequence 11, Appl
43	81.6	5.4	1260	4	US-08-745-995A-16	Sequence 16, Appl
44	81.6	5.4	1260	4	US-08-745-995A-17	Sequence 17, Appl
45	81.6	5.4	1358	4	US-08-745-995A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-023-173-10
; Sequence 10, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; TITLE OF INVENTION: In Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0960
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-023-173-10

Query Match 41.3%; Score 629.4; DB 3; Length 1308;
Best Local Similarity 70.8%; Pred. NO. 8.9e-154;
Matches 837; Conservative 0; Mismatches 346; Indels 0; Gaps 0;
QY 11 GGAAGACCCCTCAAGCGGACCGCTCAAAAACCGACACCATCATCACCACCAAGACCA 70
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Db 116 GGAGGACCCGCGGCGCGCGCCAGAGAGCGGACACCGACCGCCACCGACGAGACCA 175
QY 71 TCCGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACA 130
Db 176 CCGGAGGTTTCAACAAGATCACCCCGAATTTGGCCGAATTTGCGCTTCAAGCTGTACCGGCA 235
QY 131 ATTAGTCATCAAGAATAATTTACTAACAATTTTCTTCTCTGTTTCTTATTTGCCACTGC 190
Db 236 GCTCGGCGACCATCAACTCCCAACATCTTCTTACCCCGGTCAGCATGCCACCGC 295
QY 191 TTTTCGCGCATTTGAGTTTAGTTACTAAAGCCGATACCCATGACGAGATTTTGAAGGTTT 250
Db 296 CTTTCGCGCATCTGCTCCCTGGGTACCAAGGCGGACACCCACGAGATCTCGAAGGGCT 355
QY 251 AACTTTTAATTTGACCGAATCCCAAGCCCAATTTACGAGGGTTTTCAGAGTTGTT 310
Db 356 GAACTTCAACTGACGAGATCCCGGAGCGCAGATCCACGAGGGCTTCCAGGAGTGCT 415
QY 311 GAGAACTTTCAATCAACTGATCTCAATTTGCAATTTAACTACTGTGAACGGTTTATTTT 370
Db 416 CAGGACGCTCARCGCGGACCTCCAGCTCCAGCTCACACCGGCAACGGGCTCTCTCT 475
QY 371 GTCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCGTCAAGAACTATATCATAG 430
Db 476 GTCCGAGGGCTCAAGCTCGTCGATTAAGTTCTTGAGGACGTTGAAGAAGCTTACCACTC 535
QY 431 TGAGGCTTTTACCGTTAAATTTTGGTATCTAGGAGAGCTAAAGCAATTAATGATTA 490
Db 536 CGAGGCGTTTACCGTCAACTTCGCGGACACCGGAGGAGGCAAGACGATCAACGACTA 595
QY 491 TGTGTGAAGAGGACCCAGGAGTGAAGTGTGACCTAGTTTAAAGAAATTTAGATCGTGATAC 550
Db 596 CGTCGAGAAGGACCCAGGCGAAGTCTGACCTGAGTCTGACCTGCTCAAGAAATTTGACAGG 655
QY 551 CGCTTCGCGCACTAGTTAACTATATTTTTCAGGGTAAGTGGGAAGCGTCTTTCAGGT 610
Db 656 CGTCTTCGCGCTCGTCAACTACATCTTCTTCAAGGGCAAGTGGGAGCGCGCTTCGAGGT 715
QY 611 TAAAGTACTGACGAGAGATTTTCATGTTGATCAAGTTTACTGCTCAAGTTTCCAAT 670
Db 716 GAAGGACACCGAGGAGGAGTCTTCCAGCTGCGACAGGTCCACCGCTCAAGTCCCGAT 775
QY 671 GATGAAAGAGCTGGGTATGTTCAATATTCACATTTGCAAAATTTAAGTTCTTGGGTCTT 730
Db 776 GATGAAGAGCTGGCATGTTTCAACTCCAGCACTGCAAGAAGCTCTCCACGTGGGTCT 835
QY 731 ATTAATGAAGTATTTAGTAACTGCTACTGCTATTTTCTTTTACCAGCAAGGTAAGCT 790
Db 836 CCTCATGAAGTACCTGGGGAACGCCCGGCTCTTCTTCCGCGGACGAGGCAAGCT 895
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Db 896 CCAGCACTTGAGAGACGAGCTGACGACGACATCATCACGAAGTTCTGGAGAACGAGGA 955
QY 851 TCGTGTAGCGCTTCTGACACCTGCGCAAGTTAAGTATCACCGGTACTTACGACTTAA 910
Db 956 CAGGCGCTCCGCTACGCTCCACCTCCGGAAGCTGAGCATCACCGGACGTACGACCTGAA 1015
QY 911 ATCTGTTTTCGCGAGTTAGTATTTACCAAGTTTCTTAAAGCTGCTGCTTTCAGTGG 970
Db 1016 GAGCGTGTGGGCGAGCTGGGCACTACGAGGCTCTTCCAGCAACCGCGGACCTCTCCG 1075
QY 971 TGTTACTGAAGAAGCTCCATTTAAATTTAGTAAAGCTGTTTCAAAAGCGCTTTAAGTAT 1030
Db 1076 CGTGAGGAGGAGGCGCCCTGAACTCTTCCAGGCGGCTGACAAAGCGGTGCTCAGAT 1135
QY 1031 TGATGAAGAAGGTACCGAGGCGCGCGGCTATGTTCTGGAAGCTATTTCCATGAGCAT 1090
Db 1136 CGACGAGAAGGAGGAGGAGGCTGGCGGGGCAATGTTCTGGAGGCCATCCCATGTCAT 1195
QY 1091 TCCACGAGAAGTTAAATTTAATAAACCATTCTGTTTCTGATGATGACGAGCAACTAA 1150
Db 1196 CCCGCGCGAGGTCAAGTTTCAACAGCCCTTCTCTCTGATGATGACGAGCAACAGAA 1255

QY 1151 AAGCCATTTGTTTATGGTAAAGTTGTCAACCCCAACTCAGAAG 1193
Db 1256 GAGCCCTCTTCATGGGAAGGTGCTCAACCCCAAGAGAAG 1298
RESULT 2
US-09-023-339-6
; Sequence 6, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of \1-Antitrypsin
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Denlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,339
; FILING DATE: 13-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,991
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 0665-0003.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized No. 61271451/XhoI fragment encoding Ramy3D
; CLONE: signal peptide-AAT fusion protein
; US-09-023-339-6

Query Match 41.3%; Score 629.4; DB 3; Length 1308;
Best Local Similarity 70.8%; Pred. No. 8.9e-154;
Matches 837; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

QY 11 GAAGACCCCTCAAGGCGAGCGCGCTCAAAAACCGCACCGCTCATCAGACCAAGACCA 70
Db 116 GGAGGACCCGCGGCGGCGCGCCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 175
QY 71 TCCGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACA 130
Db 176 CCGGAGGTTTCAACAAGATCACCCCGAATTTGGCCGAATTTGCGCTTCAAGCTGTACCGCA 235
QY 131 ATTAGTCATCAAGAATAATTTACTAACAATTTTCTTCTGTTTCTTATTTGCCACTGC 190
Db 236 GCTCGGCGACCATCTCCAACTCCACCAACATCTTCTTACGCCGGTGAGCATCGCACCCG 295
QY 191 TTTTCGCGCATTTGAGTTTAGTTAGTACTAAAGCCGATACCCATGACGAGATTTTGAAGGTTT 250
Db 296 CTTTCGCGCATCTGCTCCCTGGGTACCAAGGCGGACACCCACGAGATCTCTGAAGGGCT 355
QY 251 AACTTTTAATTTGACCGAATCCCAAGCCCAATTTACGAGGGTTTTCAGAGTTGTT 310

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Db 356 GAACCTTCAACCTGACGGAGATCCCGGAGCGAGATCCACGAGGCTCCAGAGCTGCT 415
QY 311 GAGAACTTTGAATCAACCTGATTTCTCAATTTGCAATTTAACTACTGTGTAAGCGTTTATTTTT 370
Db 416 GAGAGAGCTCAACGAGCGGACTCCCGAGCTCCAGCTCAGCTCAGCCGCAACGGGCTCTTCT 475
QY 371 GTCTGAAGGTTTAAATTTGTTGACAAATTTCTAGAGAGCTCAAGAACTATATCATAG 430
Db 476 GTCCGAGGGCTCAAGCTGCTGATTAAGTTCTTGAGGAGCTGAAGAAGCTCTACCACTC 535
QY 431 TGAGGCTTTTACCGTTTAAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAAATTAATGATTA 490
Db 536 CGAGGGGTTTACCGTTTCAACTTCGGGACACCGGAGGCGCAAGAGAGATCAAGGACTA 595
QY 491 TGTGTGAAGAGGACCCAGGTTAAGATCTTCACTAGTTTAAAGAAATTAGATCGTGATAC 550
Db 596 CGTGAAGAGGGGACCCAGGGAAGATCTGAGCCTGCTCAAGGAATTTGGACGGAGAC 655
QY 551 CGTCTTCGCACTAGTTTAACTATATTTTCAAGGTTAAGTGGGAACGCTCTTTCGAGGT 610
Db 656 CGTCTTCGCGCTCGTCAACTACATCTTCTCAAGGCGAAGTGGGAGCGCCCGTTCGAGGT 715
QY 611 TAAAGATCTGAAGAGGAGATTTTCAATTTGATCAAGTTACTACTGTCAAAAGTTCCAAAT 670
Db 716 GAAGGACACCGGAGGAGGAGCTCCAGCTCGACAGGTCACCAAGCTCAAGGTCCTCCGAT 775
QY 671 GATGAAGAGCTGGGTATCTTCAATTTCAACATTTGCAAAATTAAGTTCTTGGGTCTT 730
Db 776 GATGAAGAGCTCGGATGTTTCAACATCCAGCAGTCAAGAAAGCTCTCCAGCTGGGTGCT 835
QY 731 ATTAATGAAGTATTTAGTTAAGCTACTGCTATTTTTTTTACGAGACGAAGTAAGCT 790
Db 836 CTTATGAAGTACCTGGGGAAGCGCCAGCTCTTCTTCTCGCGGAGGAGGCAAGCT 895
QY 791 TCACATTTAGAGATGAGTTGACTGATCATGACATTAATTAATTTTAAAGAAACGAGGA 850
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QY 851 TCGTCTGAGCGCTTCTGTCACCTTCCCAAGTTAAGTATCAACGCTACTTACGACTTAA 910
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QY 911 ATCTGTTTATGCGGAGTTAGTATTAACAAAGTTTCTTAAAGGTCGCGATTTGAGTG 970
Db 1016 GAGCGTGTGGGCGAGCTGGGATCACGAAGTCTTCAGCAACGCGCGGACCTCTCCG 1075
QY 971 TGTACTGAAGAGCTCCATTAATTAAGTAAAGCTGTTTCAAAAGCGGCTTAACTAT 1030
Db 1076 CGTGAGGAGGAGGCGCCCTGAGCTCTCAAGGCGGTGCAACAGCGGTGCTCAAGAT 1135
QY 1031 TGATGAAGAGGTACCGAGGCGCGGCGCTATGTTCTGGAAGCTATTTCAATGAGCAT 1090
Db 1136 CGACGAGAAGGAGGAGGAGCTGCGCGGCGCATGTTCTTGAGGCGCATCCCATGTCAT 1195
QY 1091 TCCACCAAGCTTAAATTTAATTAACCATGCTGTTTTTCTGATGATGAGAGCAACTAA 1150
Db 1196 CCGGCGGAGGCTCAAGTTTCAACAAAGCGCTTCTGTTCTCTGATGATGAGAGCAAGCA 1255
QY 1151 AAGCCATTTGTTATGGTAAAGTTGTCAACCCCAACTCAAG 1193
Db 1256 GAGGCGCTCTCATGGGAGGCTGCTCAACCCCGAGAG 1298
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RESULT 3

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US-09-023-339-3
; Sequence 3, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of '1-Antitrypsin
; TITLE OF INVENTION: in Plants
```

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; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 50850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,339
; FILING DATE: 13-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,991
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 0665-0003.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0960
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized AAT coding sequence
US-09-023-339-3
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Query Match 41.2%; Score 628.4; DB 3; Length 1185;
Best Local Similarity 70.7%; Pred. No. 1.6e-153;
Matches 836; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

QY 12 GAAGACCTTCAAGGCGAGCGCGCTCAAAAACCGACACCATCATCACGACCAAGACCAT 71
Db 1 GAGGACCGCGAGGCGCGCGCGCGAGAGAGACCGACACGACGACGACGACGACGAC 60
QY 72 CGGACTTTTATATAAATTTACTTCCAAAATTTAGCCGAATTTGCTTTTGTATAGACAA 131
Db 61 CGAGCTTTTCAACAAGATCACCGCGAATTTGGCGCAATTCGCTTCAGCCTGTACCGCGAG 120
QY 132 TTAGCTCATCAAGTAAATTTCTACTTAACATTTTTTTTAGTCTGTTCTATTGCGCACTGT 191
Db 121 CTCGGCAGCAGTCCAACTCCCAACATCTTCTTACGCGCGGTGAGCATCGCCACGCGC 180
QY 192 TTCGCCATGTTGAGTTTAGTACTTAAAGCGGATACCCCATGACGAGATTTTGAAGGTTTA 251
Db 181 TTCGCCATGTTGTTCCCTGGGTACCAGGCGGAGACACCCACGAGATCTCTCGAAGGCTG 240
QY 252 AACTTTAATTTGACGGAATTTCCAGAGAGCCCAATTTACGAGGGTTTTCAGAGTTGTTG 311
Db 241 AACTTTAACCCTGAGGAGATCCCGGAGGCGAGATCCACGAGGCGCTTCCAGGAGCTGCTC 300
QY 312 AGAAGCTTTGAATCAACCTGATTTCTCAATTTCAATTTACTACTGTACGTTATTTTTT 371
Db 301 AGGAGCTCAACAGCGCGGACTCCAGCTCCAGCTCCAGCTCCAGCGCAACGCGGTCTTCTC 360
QY 372 TCTGAAGTTTAAATTTGGTTGACAAATTTCTAGAAGAGCTCAAGAACTATATCATAGT 431
Db 361 TCCGAGGCGCTCAAGCTCGTCGATAAGTTCTCTGAGGAGCTGGAAGAGCTCTACCACTCC 420
QY 432 GAGGCTTTTACCCTTAATTTTGGTGATGATGAGAGAGCTTAAAGCAAAATTAATGATAT 491
Db 421 GAGCGGTTTACCGCTCAACTTTCGGGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 492 GTTGAGAAAGGCGACCCAGGTTAAGTGTGACCTAGTTTAAAGAAATTTAGATCGTGATACC 551
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Db	481	GTGGAAGAGGGACCCAGGCGAAGATCGTGGACCTGGTCAAGGAATTTGGACAGGGACACC	540
Qy	552	GTCTTCGCACCTAGTTAACTATATATTTTTTCAAGGGTAAGTGGGAAGCTTCCTTTCCGAGGTT	611
Db	541	GTCTTCGGCTCGTCAACTACATCTCTTCAAGGGCAAGTGGAGCGCCGTTTCGAGGTG	600
Qy	612	AAAGATACTGAAGAGGAGATTTTCATGTTGATCAAGTTTACTACTCTCAAAGTTCCAAATG	671
Db	601	AAGGACACCGAGGAGGAGACTTCCACGTCGACCAAGTCAACACCGTCAAGTCCCGATG	660
Qy	672	ATGAAAGACTGGGTATGTTCCAAATATTCAACATTTGCAAAAAATTAAGTTCTTGGGTCTTA	731
Db	661	ATGARAGGCTCGGCATGTTCAACATCCAGCACTGCAAGAAGCTCTCCAGCTGGGTGCTC	720
Qy	732	TTAATGAAGTATTAGGTAACGGCTACGTCTATTTTTTTTACCAGACCAAGGTAAGCTT	791
Db	721	CTCATGAAGTACTGGGGAACCGCACCGCCATCTTCTTCGCGGACAGGGCAAGCTC	780
Qy	792	CAACATTTAGAGAAATGAGTTCGACTCATGACATATTACTAAATTTTTAGAGAACAGGAT	851
Db	781	CAGCACTGGGAACAGACTCAGCAGCAGCATCATCAGAAATTCTCTGGAGAACAGGAGC	840
Qy	852	CGTCGTAGCGCTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTTACGACTTAAAA	911
Db	841	AGCGCTCGCTAGCTCCACCTCCCGAAGCTGAGCATCACCGGCACGTACGACCTTGAAG	900
Qy	912	TCGTGTTTTAGGCCAGTTAGGTATTACCAAACTTTTTTCTAACGCTGCCGATTTGAGTGT	971
Db	901	AGCGTGCTGGGCGAGCTGGGCATCAGAAAGTCTTTCAGCAACGGCGGGACCTCTCCGCG	960
Qy	972	GTTTACTGAAGAAGCTCCATTAAATTTGAGTAAAGCTGTTCAAAAGCCGCTCTTAAGTAT	1031
Db	961	GTGACGGAGAGGCCCCCTGAAAGCTCTCCAAGGCCGTGCAAGGCCGTGCTCAGATC	1020
Qy	1032	GATGAAGAAGGTTACCGAGGCCCGCGGCTATGTTCTCTGGAAAGCTATTCCAATGAGCAT	1091
Db	1021	GACGAGAAGGGGACGGAAGCTCCGCGGGCCATGTTTCTCTGGAGGCCATCCCATGTCCATC	1080
Qy	1092	CCACCGAAGCTTAAATTTAATAAAGCATTCGTTTTTCTGTATGTCGAGCAGAACACTAAA	1151
Db	1081	CCGCCCGAGGTCAAGTTCACAAAGCCCTTCGTCTCTCTGATGATCGAGCAGAACCAAG	1140
Qy	1152	AGCCCATGTTTATGGGTATAGGTTGTCACCCCACTCAGAAG	1193
Db	1141	AGCCCCCTCTTTCATGGGAGAGTCTGTCACCCCGCAGAGAAG	1182

RESULT 4	
US-09-023-173-5	
; Sequence 5, Application US/09023173	
; Patent No. 6066781	
; GENERAL INFORMATION:	
; APPLICANT: Sutliff, Thomas D.	
; APPLICANT: Rodriguez, Raymond L. of Mature Proteins	
; TITLE OF INVENTION: Production of Mature Proteins	
; TITLE OF INVENTION: in Plants	
; NUMBER OF SEQUENCES: 23	
; CORRESPONDENCE ADDRESS:	
; ADDRESS: Dehlinger & Associates	
; STREET: 350 Cambridge Ave., Suite 250	
; CITY: Palo Alto	
; STATE: CA	
; COUNTRY: USA	
; ZIP: 94306	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Diskette	
; COMPUTER: IBM Compatible	
; OPERATING SYSTEM: DOS	
; SOFTWARE: FastSeq for Windows Version 2.0	
; CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/09/023,173	
; FILING DATE: 13-FEB-1998	

972	QY	GT	TACTGAAGAGCTCCATTTAAATTTAGATTAAGCTGTTCCAAAGCCGCTTAACTATT	1031
961	Db	GT	CACAGAGGAGGCCACCCCTGAAGCTCTCCAAGGCCGTGATTAAGCTGTGCTGACCATC	1020
1032	QY	GAT	GAAGAAGGTACCGAGGCCGCGCGGCGCTATGTTCTCTGGAAGCTATTCCAATGAGCAATT	1091
1021	Db	GAC	GAGAAGGACATGAAGCTGCTGGGGCCATGTTTTAGAGGCCATACCCATGCTATC	1080
1092	QY	CC	ACCAGAAGTTAAATTTAATAAACCATTTCGTTTTCTGATGATCGAGCAGACACATAA	1151
1081	Db	CCCC	CGAGGTCAAGTTTCAACAACCCCTTTGCTCTCTTAATGATTGAACAAAATACCAAG	1140
1152	QY	AG	CCCATGTTTATGGGTAAGTTGTCAACCCCACTCAGAA	1192
1141	Db	TC	TCCCTCTTTCATGGGAAAAGTGTGAATCCCAACCCAAAA	1181

RESULT 6

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US-09-299-141-4
; Sequence 4, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5932
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p43C-AT
US-09-299-141-4

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Query Match      28.1%; Score 429; DB 4; Length 5932;
Best Local Similarity 60.2%; Pred. No. 1.1e-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;
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Qy	12	GAGACCCCTCAAGCGACGCCCTCAAAAACCCGACACCACTCATCAGCACCAAGACCAT	71
Db	1385	GAGATCCCCAGGGAGATGCTCCCGAAGACAGATACATCCCACTGATGATCAGGATCAC	1444
Qy	72	CCGACTTTTAAATAAAATTACTCCAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA	131
Db	1445	CCAACTTTCAACAGATATACCCCAACCTGGCTGATTCGCTTCAGCTTATACGCCAG	1504
Qy	132	TTAGCTCATCAAAAGTAATTCTACTAACATTTTTTTTTTAGTCCTGTTTCTATTGCCACTGCT	191
Db	1505	CTGGCACACCAGTCCAACAGCACCAATATCTTCTCTCCCACTGAGCATCGTACAGCC	1564
Qy	192	TTGCCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGRAGGTTTA	251
Db	1565	TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTACGATGAATTCCTGGAGGGCGTG	1624
Qy	252	AACTTTAAITTGACCGNAATCCACAGAAGCCCAAAATTCACGAGGTTTTTCAAGAGTTTGTG	311
Db	1625	AAITTCAACTCATCGGAGATTCCGGAGGCTCAGATCCAGTAAGGCTTCCAGGAACCTCTC	1684
Qy	312	AGAACTTTGAATCAACCTGATTCTCAATTTGCAATTTAACTACTGTGTAAACGGTTATTTTGTG	371
Db	1895	CGTACCTCAACCAAGCAGACAGCCAGCTCCAGCTCACCACCGCAATGGCCTGTCTCCTC	1744
Qy	372	TCTCAAGGTTTAAATTTGGTTGACAATTTCTTAGAAGAGCTCAAGAACTATATCATAGT	431
Db	1745	AGCCAGGCGCTGAAGCTAGTGGATAGTTTTTTGGAGGATGTTTAAAAGTTGTACCACTCA	1804

RESULT 7

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RES001:
/ 09/299-141-8
/ Sequence 8, Application US/09299141
/ Patent No. 6461606
/ GENERAL INFORMATION:
/ APPLICANT: FLOTTE, TERENCE R.
/ APPLICANT: SONG, SIHONG
/ APPLICANT: BYRNE, BARRY J.
/ APPLICANT: MORGAN, MICHAEL
/ TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
/ FILE REFERENCE: 4300.011800
/ CURRENT APPLICATION NUMBER: US/09/299,141
/ CURRENT FILING DATE: 1999-04-23
/ EARLIER APPLICATION NUMBER: 60/083,025
/ EARLIER FILING DATE: 1998-04-24
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 6142

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Mon Dec 9 12:50:34 2002

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; SEQ ID NO 6
; LENGTH: 6714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PLASMID
; OTHER INFORMATION: p43CB-AT
US-09-299-141-6

Query Match      28.1%; Score 429; DB 4; Length 6714;
Best Local Similarity 60.2%; Pred. No. 1.le-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGACCGCTCAAAACCGACACACGATCATCAGACCAAGACCAT 71
Db 2167 GAGGATCCCGAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGATCAC 2226
QY 72 CGGACCTTTAATAAATAATCTCCAAATTTAGCGGAATTTGCTTTTCTTTGATAGACAA 131
Db 2227 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTGCGCTTACGCCATATACGCCAG 2286
QY 132 TTAGCTCATCAAGTAATTTCTACTAATATTTTCTTTAGTCTCTGTTTCTATTGCCACTGT 191
Db 2287 CTGGCACACCGAGTCCCAACAGACACCAATATCTTCTCTCCAGTGAGCATCGCTACAGCC 2346
QY 192 TTCGCCATGTTGAGTTTAGTACTAAAGCCGATPACCCATGACAGATTTTAGNAGGTTTA 251
Db 2347 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGATGAAATCTGGAGGCGCTG 2406
QY 252 AACTTTAATTTGACCGAATCCCGAAGCCCAATTCAGAGGGTTTTCAGAGAGTTTGTG 311
Db 2407 AATTTCACCTCAGGAGATTCGGGAGGCTCAGATCCATGAAAGTTTGTGAGGCTCTC 2466
QY 312 AGACTTTGATCAACCTGATTTCTCAATTCGAATTAAGTACTGTTAAACGGTTTATTTTG 371
Db 2467 CGTACCTCAACCGAGCCAGACAGCCACCTCGAGTGCACCGCCGAATGGCTGTCTC 2526
QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAACGTCAGAACTATATCATAGT 431
Db 2527 AGCGAGGCGCTGAAGCTAGTGGATAAGTTTGTGAGGATGTTTAAAGTTTGTACCATCA 2586
QY 432 GAGGCTTTTACCGTTAATTTTGGTGTACTGAGGAAGCTTAAAGCAAAATTAATGATTAT 491
Db 2587 GAAGCCTTCACTGTCACTCGGGGACACCGAAGGCCAAGAACAGATCAACGATTAC 2646
QY 492 GTTGAAGAAGCCACCGGTAAGATCGTTCACCTAGTTTAAAGAAATTTAGATCGTATACC 551
Db 2647 GTGGAGAAGGTTACTCAAGGGAAAATTTGGATTGTTGTCGAAGGAGCTTGACAGAGACA 2706
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGTAAGTGGGAACGTCCTTTTCGAGGTT 611
Db 2707 GTTTTGTCTGTTGAATTTACATCTTCTTAAAGGCAATGCCACCGCATCTCTCTGAGTC 2766
QY 612 AAAGATACCTGAGAGGAAGATTTTTCATGTTCAAGTTACTACTGTCTCAAAAGTTCCAAATG 671
Db 2767 AAGGACACCGGAGGAAGAGCTTCCAGTGGACAGGTCACCCGTCGAAGTGCCTATG 2826
QY 672 ATGAAAAGACTGGGTATGTTCAATATTCACATTCGAAAATTAAGTTCTTGGGCTTTA 731
Db 2827 ATGAACCGTTTAGGCATGTTTAAACATCCAGCAGCTGTAAGAAGCTGCCAGCTGGGTGCTG 2886
QY 732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTATTTTACCAGAGGAAGTAAAGTT 791
Db 2887 CTGATGAAATACCTGGGCAATGCCACCGCATCTCTCTCTGCTGATGAGGGAACATA 2946
QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATATTTACTAAATTTTATAGAACAGGAT 851
Db 2947 CAGCACTGGAAATGAATCACTCACCACGATATCATCACCAGATTCCTGGAATGAAGAC 3006
QY 852 CGTCGTAGCGCTTCTCTGCACTGCGCAAGTTAAGTATCACCAGTACTTACCACTTAAA 911
Db 3007 AGAAGGCTGCCAGCTTACATTTTACCCAACTGTCCTCACTTGAACCTATGATCTGAAG 3066
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; SEQ ID NO 6
; LENGTH: 6714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PLASMID
; OTHER INFORMATION: p43CB-AT
US-09-299-141-6

Query Match      28.1%; Score 429; DB 4; Length 6714;
Best Local Similarity 60.2%; Pred. No. 1.le-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGACCGCTCAAAACCGACACACGATCATCAGACCAAGACCAT 71
Db 2167 GAGGATCCCGAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGATCAC 2226
QY 72 CGGACCTTTAATAAATAATCTCCAAATTTAGCGGAATTTGCTTTTCTTTGATAGACAA 131
Db 2227 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTGCGCTTACGCCATATACGCCAG 2286
QY 132 TTAGCTCATCAAGTAATTTCTACTAATATTTTCTTTAGTCTCTGTTTCTATTGCCACTGT 191
Db 2287 CTGGCACACCGAGTCCCAACAGACACCAATATCTTCTCTCCAGTGAGCATCGCTACAGCC 2346
QY 192 TTCGCCATGTTGAGTTTAGTACTAAAGCCGATPACCCATGACAGATTTTAGNAGGTTTA 251
Db 2347 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGATGAAATCTGGAGGCGCTG 2406
QY 252 AACTTTAATTTGACCGAATCCCGAAGCCCAATTCAGAGGGTTTTCAGAGAGTTTGTG 311
Db 2407 AATTTCACCTCAGGAGATTCGGGAGGCTCAGATCCATGAAAGTTTGTGAGGCTCTC 2466
QY 312 AGACTTTGATCAACCTGATTTCTCAATTCGAATTAAGTACTGTTAAACGGTTTATTTTG 371
Db 2467 CGTACCTCAACCGAGCCAGACAGCCACCTCGAGTGCACCGCCGAATGGCTGTCTC 2526
QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAACGTCAGAACTATATCATAGT 431
Db 2527 AGCGAGGCGCTGAAGCTAGTGGATAAGTTTGTGAGGATGTTTAAAGTTTGTACCATCA 2586
QY 432 GAGGCTTTTACCGTTAATTTTGGTGTACTGAGGAAGCTTAAAGCAAAATTAATGATTAT 491
Db 2587 GAAGCCTTCACTGTCACTCGGGGACACCGAAGGCCAAGAACAGATCAACGATTAC 2646
QY 492 GTTGAAGAAGCCACCGGTAAGATCGTTCACCTAGTTTAAAGAAATTTAGATCGTATACC 551
Db 2647 GTGGAGAAGGTTACTCAAGGGAAAATTTGGATTGTTGTCGAAGGAGCTTGACAGAGACA 2706
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGTAAGTGGGAACGTCCTTTTCGAGGTT 611
Db 2707 GTTTTGTCTGTTGAATTTACATCTTCTTAAAGGCAATGCCACCGCATCTCTCTGAGTC 2766
QY 612 AAAGATACCTGAGAGGAAGATTTTTCATGTTCAAGTTACTACTGTCTCAAAAGTTCCAAATG 671
Db 2767 AAGGACACCGGAGGAAGAGCTTCCAGTGGACAGGTCACCCGTCGAAGTGCCTATG 2826
QY 672 ATGAAAAGACTGGGTATGTTCAATATTCACATTCGAAAATTAAGTTCTTGGGCTTTA 731
Db 2827 ATGAACCGTTTAGGCATGTTTAAACATCCAGCAGCTGTAAGAAGCTGCCAGCTGGGTGCTG 2886
QY 732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTATTTTACCAGAGGAAGTAAAGTT 791
Db 2887 CTGATGAAATACCTGGGCAATGCCACCGCATCTCTCTCTGCTGATGAGGGAACATA 2946
QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATATTTACTAAATTTTATAGAACAGGAT 851
Db 2947 CAGCACTGGAAATGAATCACTCACCACGATATCATCACCAGATTCCTGGAATGAAGAC 3006
QY 852 CGTCGTAGCGCTTCTCTGCACTGCGCAAGTTAAGTATCACCAGTACTTACCACTTAAA 911
Db 3007 AGAAGGCTGCCAGCTTACATTTTACCCAACTGTCCTCACTTGAACCTATGATCTGAAG 3066
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; SEQ ID NO 6
; LENGTH: 6714
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PLASMID
; OTHER INFORMATION: p43CB-AT
US-09-299-141-6

Query Match      28.1%; Score 429; DB 4; Length 6714;
Best Local Similarity 60.2%; Pred. No. 1.le-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGACCGCTCAAAACCGACACACGATCATCAGACCAAGACCAT 71
Db 2167 GAGGATCCCGAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGATCAC 2226
QY 72 CGGACCTTTAATAAATAATCTCCAAATTTAGCGGAATTTGCTTTTCTTTGATAGACAA 131
Db 2227 CCAACCTTCAACAAGATCACCCCAACCTGGCTGAGTTGCGCTTACGCCATATACGCCAG 2286
QY 132 TTAGCTCATCAAGTAATTTCTACTAATATTTTCTTTAGTCTCTGTTTCTATTGCCACTGT 191
Db 2287 CTGGCACACCGAGTCCCAACAGACACCAATATCTTCTCTCCAGTGAGCATCGCTACAGCC 2346
QY 192 TTCGCCATGTTGAGTTTAGTACTAAAGCCGATPACCCATGACAGATTTTAGNAGGTTTA 251
Db 2347 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGATGAAATCTGGAGGCGCTG 2406
QY 252 AACTTTAATTTGACCGAATCCCGAAGCCCAATTCAGAGGGTTTTCAGAGAGTTTGTG 311
Db 2407 AATTTCACCTCAGGAGATTCGGGAGGCTCAGATCCATGAAAGTTTGTGAGGCTCTC 2466
QY 312 AGACTTTGATCAACCTGATTTCTCAATTCGAATTAAGTACTGTTAAACGGTTTATTTTG 371
Db 2467 CGTACCTCAACCGAGCCAGACAGCCACCTCGAGTGCACCGCCGAATGGCTGTCTC 2526
QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAACGTCAGAACTATATCATAGT 431
Db 2527 AGCGAGGCGCTGAAGCTAGTGGATAAGTTTGTGAGGATGTTTAAAGTTTGTACCATCA 2586
QY 432 GAGGCTTTTACCGTTAATTTTGGTGTACTGAGGAAGCTTAAAGCAAAATTAATGATTAT 491
Db 2587 GAAGCCTTCACTGTCACTCGGGGACACCGAAGGCCAAGAACAGATCAACGATTAC 2646
QY 492 GTTGAAGAAGCCACCGGTAAGATCGTTCACCTAGTTTAAAGAAATTTAGATCGTATACC 551
Db 2647 GTGGAGAAGGTTACTCAAGGGAAAATTTGGATTGTTGTCGAAGGAGCTTGACAGAGACA 2706
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGTAAGTGGGAACGTCCTTTTCGAGGTT 611
Db 2707 GTTTTGTCTGTTGAATTTACATCTTCTTAAAGGCAATGCCACCGCATCTCTCTGAGTC 2766
QY 612 AAAGATACCTGAGAGGAAGATTTTTCATGTTCAAGTTACTACTGTCTCAAAAGTTCCAAATG 671
Db 2767 AAGGACACCGGAGGAAGAGCTTCCAGTGGACAGGTCACCCGTCGAAGTGCCTATG 2826
QY 672 ATGAAAAGACTGGGTATGTTCAATATTCACATTCGAAAATTAAGTTCTTGGGCTTTA 731
Db 2827 ATGAACCGTTTAGGCATGTTTAAACATCCAGCAGCTGTAAGAAGCTGCCAGCTGGGTGCTG 2886
QY 732 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTATTTTACCAGAGGAAGTAAAGTT 791
Db 2887 CTGATGAAATACCTGGGCAATGCCACCGCATCTCTCTCTGCTGATGAGGGAACATA 2946
QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATATTTACTAAATTTTATAGAACAGGAT 851
Db 2947 CAGCACTGGAAATGAATCACTCACCACGATATCATCACCAGATTCCTGGAATGAAGAC 3006
QY 852 CGTCGTAGCGCTTCTCTGCACTGCGCAAGTTAAGTATCACCAGTACTTACCACTTAAA 911
Db 3007 AGAAGGCTGCCAGCTTACATTTTACCCAACTGTCCTCACTTGAACCTATGATCTGAAG 3066
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EARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 6924
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PLASMID
OTHER INFORMATION: p43rmsENCB-AT
US-09-299-141-10

Query Match 28.1%; Score 429; DB 4; Length 6924;
Best Local Similarity 60.2%; Pred. No. 1.1e-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGAGCGCGCTCAAAAAACCGACACAGTATCATCGACAGACCAT 71
DB 2377 GAGGATCCCCAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGGATCAC 2436
QY 72 CGGACTTTTAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 131
DB 2437 CCAACCTTCAACAAGATCAACCCCAACCTGGCTGAGTTTCGCTTCAGGCTATACGCGCAG 2496
QY 132 TTAGCTCATCAAGTAATTTCTACTACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 191
DB 2497 GTGGCACCAGTCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2556
QY 192 TTGCGCATGTTAGGTAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 251
DB 2557 TTTGCAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2616
QY 252 AACTTTAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGA 311
DB 2617 AATTTCAACCTCAAGGATGCTGGGAGGATGCTGGGAGGATGCTGGGAGGATGCTGGGAGG 2676
QY 312 AGAAGCTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 371
DB 2677 CGTACCTTCAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2736
QY 372 TCTGAAGGTTTAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 431
DB 2737 AGCGAGGCGCTGAAGCTAGTGGATAAGTTTGGAGGATGTTTAAAGGATGTTGTTGTTGTTGTT 2796
QY 432 GAGGCTTTTACCTTAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 491
DB 2797 GAAGCCTTCACTGTCACTTTCGGGACACGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGG 2856
QY 492 GTTGAGAAAGCGACCCAGGTAAGATGTTGACCTAGTTTAAAGAAATTAAGTCTTGGGCTTAA 551
DB 2857 GTGGAGAAGGTTACTCAAGGGAATAATTTGTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2916
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGAGGTAAGTGGGAAGCTGCTTTCGAGGTT 611
DB 2917 GTTTTGTCTGTGGTAATTAATTTCTTAAAGGCAATTTGGAGAGACCTTTGAGTTC 2976
QY 612 AAGATATCTGAAGAGGAAGATTTTCACTGTTGATCAAGTTTACTACTGTTCAAGTTTCAATG 671
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QY 672 ATGAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAATTAAGTTCTTGGGCTTAA 731
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QY 732 TTAATGAAGTATTTAGGTAAGCTTACTGCTATTTTTCAGAGGTAAGGTAAGCTT 791
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QY 792 CAACATTTAGAGAAATGAGTGTGACATGACATTAATTAATTAATTTAGAGAACGAGAT 851
DB 3157 CAGCACCTGGAAAATGAATCAACCCAGCATATCATCAACCAAGTTCTTGGAAAATGAAGAC 3216
QY 852 CGTCGTAGGCTTCTCTCGACCTGCAAGTTAAAGTATACCGGCTTACTTACGACTTAAAA 911

DB 3217 AGAAGGCTGCCAGGTTACATTTACCCAACTGTCCATTTACTGGAACCTATGATCTGAAG 3276
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DB 3277 AGGCTCTGGTCAACTGGGCATCACTAAGGTCTTTCAGCAATGGGGCTGACCTCTCCGGG 3336
QY 972 GTTACTGAAGAAGCTCCATTAATAATTTAGTAAGCTGTTTCACAAAAGCCGCTCTTAACATTT 1031
DB 3337 GTCCAGAGAGGAGCACCCTGAGCTCTCCAAGGCGGTGCATAAGGCTGTGCTGACCATC 3396
QY 1032 GATGAAAAGGTACCGAGGCGCGCGGTATGTTCTTCTGGAAGCTATTCCAATGAGCATTT 1091
DB 3397 GAGCAGAGAAGGACTGAAGCTGCTGGGCCATGTTTTTAGAGGCCATACCCATGCTATC 3456
QY 1092 CCACCCAGAGCTTAAATTTAATAAACCATTCGTTTTTCTGATGATCAGCAGACACATAA 1151
DB 3457 CCCCCGAGTCAAGTTCAACAAAACCTTTGTTCTTCTTAATGATTGAACAAAATATCCAAG 3516
QY 1152 AGCCCATGTTTATGGTAAGTTGTCAACCCCAACTCAGAA 1192
DB 3517 TCTCCCTCTTCTATGGGAAAAGTGGTGAATCCCAACCCAAAA 3557
RESULT 12
US-09-299-141-11
Sequence 11, Application US/09299141
Patent No. 6461606
GENERAL INFORMATION:
APPLICANT: FLOTTE, TERENCE R.
APPLICANT: SONG, SIHONG
APPLICANT: BYRNE, BARRY J.
APPLICANT: MORGAN, MICHAEL
TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
FILE REFERENCE: 4300.011800
CURRENT APPLICATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/083,025
EARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 6924
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PLASMID
OTHER INFORMATION: p43rmsENCB-AT
US-09-299-141-11
Query Match 28.1%; Score 429; DB 4; Length 6924;
Best Local Similarity 60.2%; Pred. No. 1.1e-101;
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGGCGAGCGCGCTCAAAAAACCGACACAGTATCATCGACAGACCAT 71
DB 2377 GAGGATCCCCAGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGGATCAC 2436
QY 72 CGGACTTTTAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 131
DB 2437 CCAACCTTCAACAAGATCAACCCCAACCTGGCTGAGTTTTCGCTTCAGGCTATACGCGCAG 2496
QY 132 TTAGCTCATCAAGTAATTTCTACTACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 191
DB 2497 GTGGCACCAGTCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2556
QY 192 TTGCGCATGTTAGGTAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 251
DB 2557 TTTGCAATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2616
QY 252 AACTTTAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGAATTTAGCGA 311
DB 2617 AATTTCAACCTCAAGGATGCTGGGAGGATGCTGGGAGGATGCTGGGAGGATGCTGGGAGG 2676

QY 312 AGAAGCTTTGAATCAACCTGATCTCAATTCGAATTAACCTACTGGTAACGGTTATTTTTC 371
Db 2677 CGTACCTCAACAGCAGACAGCCAGCTCCAGCTGACACCGCAATGGCTGTTCCTC 2736
QY 372 TCTGAAGTTTAAATTTGGTTGACAAATTCCTAGAGAGCTCAAGAAATATATATAGT 431
Db 2737 AGCGAGGCTGAAGCTAGTGGATAAGTTTGGAGGATGTTAAAGTTGTACCACTCA 2796
QY 432 GAGGCTTTTACCGTTAATTTTGGTGATCTAGGAGGCTAAAGCAATTAATGATTAT 491
Db 2797 GAAGCTTTCACCTGCTCACTTCGGGACACCGAGAGGCCAAGAAACAGATCAACGATTAC 2856
QY 492 GTTGAGAAAGGACCCAGGCTGAAGTTCGTTGACCTAGTTTAAAGAAATAGATCGTATACC 551
Db 2857 GTGGAGAGGGTACTCAAGGGAAATTTGGATTTGGTCAAGGACCTTGACAGACACA 2916
QY 552 GTCCTCGCACTAGTTAACTATATTTTTCAGGGAAGTGGGAAGCTTCCTTTTCAGGTT 611
Db 2917 GTTTTTCCTGCTGGTGAATTTACATCTCTTTAAAGGCAATGGAGAGACCCCTTTGAAGTC 2976
QY 612 AAAGATCTGAAGAGGAGATTTTCAATTTCAACATTTCAACAAATTAAGTTCTTTGGTCTTA 731
Db 2977 AAGCACCGAGAGAGGACTTCCAGCTGGACCAAGGTGACCCCGTGAAGGTGCTATG 3036
QY 672 ATGAAGACTGGGTATGTTCAATTTCAACATTTCAACAAATTAAGTTCTTTGGTCTTA 731
Db 3037 ATGAAGCTGTTAGGATGTTTAACTCCAGCACTGTAAGAGCTGTCACAGCTGGGTCTG 3096
QY 732 TTAATGAAGTATTAAGTAAAGCTACTCTATTTTTCAGAGAGGAAAGTTTCAAGGTT 791
Db 3097 CTGATGAATACCTGGGCAATGGCCACCCCATCTCTTCTTCCTGCTGATGAGGGGAACTA 3156
QY 792 CAACATTTAGAGATGAGTGTACTCATGACATTTACTAAATTTTACAGAGAGGAAAGT 851
Db 3157 GAGCACTGGAAATGAATCAACCAAGTATCATCAACCAAGTTCTTGGAAATGAAGAC 3216
QY 852 GTCCTAGCGCTTCTCGCACTGCGCAAGTTAAGTATCAACCGTACTTACGACTTAAAT 911
Db 3217 AGAAGGCTCGCAGCTTACATTTACCAAACTGTCCATTAAGTGAACCTATGATCTGAAG 3276
QY 912 TCTGTTTGAAGCTAGTATAGTATTAACCAAGTTTTCACGCTGCGGATTTGAGTGGT 971
Db 3277 AGCGTCTGGTCACTGGGATCACTAGGCTCTTCAGCAATGGGCTGACCTCTCCGGG 3336
QY 972 GTTACTGAAGAGTCCATTAATTAATTAAGTAAAGCTGTCACAAAGCGCTCTTAACATTT 1031
Db 3337 GTCACAGAGGAGGACCCCTGAAGCTCTCCAAGCGCTGCATAGGCTGTGCTGACCATC 3396
QY 1032 GATGAAGAGGTACCGAGGCGCGCGGCTATGTTCTCGGAAGCTATTCGAATGAGCAT 1091
Db 3397 GACGAGAAAGGAGTGAAGCTGCTGGGGCCATGTTTTCAGAGGCAATACCATGCTCTATC 3456
QY 1092 CCACGAGAGTTAAATTAATTAACCAATTCGTTTTCCTGATGATCGAGAGACACTAAA 1151
Db 3457 CCCCCGAGGTCAAGTTCAACAAACCTTGTCTCTTAATGATTGAACAAATACCAAG 3516
QY 1152 AGCCCATTTTATGGGTAGGTTGTCAACCCCACTCAGAA 1192
Db 3517 TCTCCCTCTTCATGGGAAAGTGTGAATCCCAACCCCAAA 3557

RESULT 13

US-09-299-141-7

; Sequence 7, Application US/09299141

; Patent No. 6461606

; GENERAL INFORMATION:

; APPLICANT: FLOTTE, TERENCE R.

; APPLICANT: SONG, SIHONG

; APPLICANT: BYRNE, BARRY J.

; APPLICANT: MORGAN, MICHAEL

; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

; FILE REFERENCE: 4300.011800

; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7
; LENGTH: 6981
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PLASMID C-AT2
US-09-299-141-7

Query Match 28.1%; Score 429; DB 4; Length 6981;

Best Local Similarity 60.2%; Pred. No. 11e-101;

Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

QY 12 GAAGACCTCAAGCGGAGCGGCTCAAAAACCGACACCAAGTATCATACGACCAAGACCAT 71
Db 165 GAGATCCCCAGGGAGATGCTGCCAGAGACAGATACATCCCACCATGATCAGGATCAC 224
QY 72 CCGACTTTTAAATAAAATTTACTCCAAATTTAGCCGAATTTTCTTTTGTATAGACAA 131
Db 225 CCAACCTTCAACAGATCACCCCAACCTGGCTGAGTTCCGCTTCAGCCTTATACGCCAG 284
QY 132 TTAGCTCATCAAGTAATTTCTACTTAACATTTTTTTTAGTCTCTTTTCTATTGGCAGTGT 191
Db 285 CTGSCACACAGTCCAAACAGCACAATATCTTCTTCTCCCACTGAGCATCGCTACAGCC 344
QY 192 TTGCGCATTTGAGTTTGGTACTAAAGCGGATACCCATGACGAGATTTTAGAAGTTTA 251
Db 345 TTTGCAATGCTCTCCCTTGGGGACCAAGGCTGACACTCACGATGAAATCTCTGGAGGCC 404
QY 252 AACTTTAATTTGACCGAAATCCCAAGAGCCCAATTTCAAGAGGTTTCAAGAGTTGTTG 311
Db 405 AATTTCAACCTCAGGAGATTCGAGGCTCAGATCCATGAGGCTTCCAGGACTCCTC 464
QY 312 AGAATTTGAATCAACCTGATTTCTCAATTTGCAATTAACCTACTGGTAAACGGTTTAT 371
Db 465 CGTACCTCAACAGCAGCAGACAGCCAGCTCCAGCTGACCAACCGGCAATGGCTTGTCTC 524
QY 372 TCTGAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCTCAAGAACTATATCATAGT 431
Db 525 AGCGAGGCTGAGCTAGTGAATAGTTTGGAGGATGTTTAAAGGTTGTACCACTCA 584
QY 432 GAGCTTTTACCGTTAATTTTGGTGTACTGAGGAAGCTTAAAGCAATTAATGATTAT 491
Db 585 GAAGCTTCTACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAACAGATCAACGATTAC 644
QY 492 GTTGAGAAAGGACCCAGGTAAGATCTGTGACCTAGTTTAAAGAAATAGATCGTATACC 551
Db 645 GTGGAAGAGGTAATCAAGGGAATTTGGGATTTGGTCAAGGAGCTTGACAGAGACACA 704
QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGGTAAAGTGGGAAGCTCTCTTCGAGTT 611
Db 705 GTTTTTCCTGCTGATGATTTTACATCTCTTAAAGCAATGGAGAGACCTTTGAAGTC 764
QY 612 AAGATGATGAAGAGAGATTTTTCATGTTGATCAAGTACTGCTCAAGTTTCAAGT 671
Db 765 AAGGACCCGAGGAAGGACTTCCACGTTGGACCAAGTGGTCAAGGAGCTTGAGGTGCTATG 824
QY 672 ATGAAAGACTGGGTATGTTCAATATTTCAACATTTCAAAAAATTAAGTTCTTGGTCTTA 731
Db 825 ATGAAGCTTTAGGATGTTTAAACATTCAGCACTGTTAAAGAGCTCTCCAGCTGGGTGCTG 884
QY 732 TTAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTTTACCAAGCAAGGTAAGCTT 791
Db 885 CTGATGAATACCTGGGCAATGCCACCCCACTCTTCTTCTCCCTGATGATGAGGGAAC 944
QY 792 CAACATTTAGAGAAAGTGTGACTCATGACATTTACTTAATTTTATAGAACAGGAT 851
Db 945 CAGCACCTGGAAATGAACCTCACCACGATATCATCACCAAGTCTCTCGAAAAATGAAGAC 1004

QY	852	CGTCGTAGCGCTTCTCTGCGACCTGCCAAAGATTAAAGTATACCGCGTACTTACGACTTAAAA	911
Db	1005	AGAAGGCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACTATGATCTGAAG	1064
QY	912	TCGTGTTTAGCCAGTTAGGTATTAACCAAGTCTTTTCTAACGGTGCAGGTTTGAAGTGT	971
Db	1065	AGCGTCTGGGTCAACTGGGCATCACTAAGGCTTACAGCAATGGGGTGACCTCTCCGGG	1124
QY	972	GTTACTGAAGAAGCTCCATTAAAAATTGAGTAAAGCTGTTACAAAAGCGGCTTTAACTATT	1031
Db	1125	GTACAGAGGAGGACCCCTGAAGCTCTCCAAGCGCGTGCATAAGAGGTGTCTGACCATC	1184
QY	1032	GATGAAAAGGTACCGAGCGCGCGCTATGTTCTGGAAGCTATTCCAATCAGCATT	1091
Db	1185	GACGAGAAAGGAGTGAAGCTGTGGGGGCCATGTTTTTAGAGGCCATACCCATGCTCTATC	1244
QY	1092	CCACCAGAAGTTAAATTAATAAACCAATTCGTTTTTCTGATGATCGAGCAACACATAAA	1151
Db	1245	CCCCCGAGGTCAAGTTCAACAAACCCCTTGTCTTCTTAATGATTGAACAAAATACCAAG	1304
QY	1152	AGCCCATTTTATGGTAAAGTTGTCAACCCAACTCAGAA	1192
Db	1305	TCTCCCTCTTATGGGAAAAAGTGGTGAATCCCAACCCCAAAA	1345
RESULT 14			
US-09-299-141-3			
; Sequence 3, Application US/09299141			
; Patent No. 6461606			
; GENERAL INFORMATION:			
; APPLICANT: FLOTTE, TERENCE R.			
; APPLICANT: SONG, SIHONG			
; APPLICANT: BYRNE, BARRY J.			
; APPLICANT: MORGAN, MICHAEL			
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY			
; FILE REFERENCE: 4300.011800			
; CURRENT APPLICATION NUMBER: US/09/299,141			
; CURRENT FILING DATE: 1999-04-23			
; EARLIER APPLICATION NUMBER: 60/083,025			
; EARLIER FILING DATE: 1998-04-24			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: PatentIn ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 7054			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:PLASMID de-AT			
US-09-299-141-3			
Query Match 28.1%; Score 429; DB 4; Length 7054;			
Best Local Similarity 60.2%; Pred. No. 1.1e-101;			
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;			
QY	12	GAAGACCCCTCAAGGGGACCGCGCTCAAAAAACCGACACAGTCATCACGACCAAGACCAT	71
Db	1433	GAGGATCCCCAGGGAGATGCTGCCAGAGACAGATACATCCACCATGATCAGGATCAC	1492
QY	72	CCGACTTTTAATAAATTACTCCAATTTAGCCGAATTTGCTTTTCTTGATATACAAA	131
Db	1493	CCAACCTTCAACAAGATCACCCCAACCTCGGTGAGTTCGCTTCAGCCTATACCCCCAG	1552
QY	132	TTAGCTCATCAAGTAATCTACTAACAATTTTTTTTAGTCTGCTTTCTATTGCGCACTGT	191
Db	1553	CTGGCACACAGTCCCAACAGCACCATATCTTCTCTCCCACTGAGCATCGCTACAGCC	1612
QY	192	TTGCCCATGTTAGTTTAGTACTAAAGCGGATACCCATGACAGATTTTAGAAGTTTA	251
Db	1613	TTTGCAATGCTCTCCCTCGGGGACCAAGGCTGACACTCAGCATGAAATCTCGGAGGCGCT	1672
QY	252	ACCTTTAATTGACCGAAATTCACAGAGGCCAAATTCACAGAGGTTTTTCAAGAGTTGTTG	311

FILE REFERENCE: 4300.011800
CURRENT APPLICATION NUMBER: US/09/299,141
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/083,025
EARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 7405

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: PLASMID E-AT
US-09-299-141-2

Query Match 28.1%; Score 429; DB 4; Length 7405;
Best Local Similarity 60.2%; Pred. No. 1.1e-101;

Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

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QY 12 GAAGACCCCTCAAGCGACCGCGCTCAAAAACCGACACCCAGTCATCACGACCAAGACCAT 71
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Db 1784 GAGGATCCCGCAGGAGATGCTGCCAGAGACAGATAGATCCACCGTATCAGGATCAC 1843

QY 72 CCCACITTTAATAAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131
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Db 1844 CCAACCTTCAACAAGATCACCCGCCAACCTGGCTGAGTTCCGCTTCAGCCATATACGCCAG 1903

QY 132 TTAGCTCATCAAGTAATTTCTACTACATTTTCTTTAGTCCCTGTTCTTATGCCACTGCT 191
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Db 1904 CTGGCACACCGATCCCAACAGCACCAATATCTTCTTCCCGAGTACGATCTACAGCC 1963

QY 192 TTGGCCATGTTGAGTTTAGTACTAAAGCCGATACCCATGACGAGATTTTGAAGGTTTA 251
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QY 252 AACTTTAATTTGACCGAATCCAGAGCCCAATTTCAAGAGGTTTTCAGAGTTGTTG 311
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QY 312 AGAAGCTTTGAATCAACCTGATTTCTCAATTTGCAATTAAGTCTGATGACGAGATTTG 371
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Db 2084 CTTACCTTCAACCCAGCCAGACAGCCAGCTCCAGTCCAGCCAGGCAATGGGCTGTCTC 2143

QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCTCAAGAACTATATCATAGT 431
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Db 2144 AGCGAGGCGCTGAAGCTAGTGGATTAAGTTTGGAGGATTTAAAGTGTGTACCACTCA 2203

QY 432 GAGGCTTTTACCGTTAATTTTGGTGATCTGAGGAGCTAAAGCAATTAAGTATTAATGAT 491
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Db 2204 GAAGCTTCACTGTCACTTCGGGACACCCGAAGAGGCCAAGAACAGATCAAGGATTA 2263

QY 492 GTTGAGAAAGGACCCAGGGTAAAGATCGTTGACCTAGTTAAAGAAATTAGATCGTGATAC 551
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Db 2264 GTGAGAAAGGGTACTCAAGGGAAATTTGCTGATTTGGTCAAGGAGCTTGACAGAGACAC 2323

QY 552 GTCTTCGCACTAGTTAACTATATTTTTCAGGGTAAAGTGGGAACTGCTTTTCAGGTT 611
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Db 2324 GTTTTGTCTGGTGAATTTACATCTTCTTTAAAGGCAATGGGAGAGACCCCTTTGAAGTC 2383

QY 612 AAAGATCTGAAGAGAGATTTTTCATGTTGATCAAGTTACTACTGTCAAGTTCCCAATG 671
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Db 2384 AAGGACCCGAGAGAGAGGACTTCCAGTGGACCGGTGACCCAGGTTGAAGGTGCGCTATG 2443

QY 672 ATGAAGAGCTGGGTATGTTCAATATTCAACATTTGCAAAAATTAAGTTCTTGGGTCTTA 731
   || || || || || || || || || || || || || || || || || || || || || ||
Db 2444 ATGAAGCGTTTGAAGCATGTTTAAACATCCAGCAGTGAAGAGCTGTCCAGCTGGGTCTG 2503

QY 732 TTAATGAAGTATTTAGTAAAGCTACTGCTATTTTTCAGAGAGAGGTAAGCTT 791
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Db 2504 CTGATGAATACCTGGGCAATGCCCGCATTTCTTCTGCTGATGAGGGAACTA 2563

QY 792 CAACATTTAGAGATGAGTTGACTCATGACATTTATTAATTTTATAGAGAACGAGGAT 851
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Search completed: December 7, 2002, 02:09:11
Job time : 87.5 secs

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Db 2564 CAGCACCTGGAATAATGAACCTACCCACGATATCATCACCAAGTTCTCTGAAAAATGAAGAC 2623
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Db 2624 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTTACTTGGAACTATGATCTGAAG 2683
QY 912 TCTGTTTTAGGCCAGTTAGGTATTACCAAAAGTTTTTTCTTAACGGTGGCGATTGAGTGGT 971
Db 2684 AGCGTCTCTGGGTCAACTGGGCATCACTAAGGTCTTTCAGCAATGGGCTGACCTCTCCGGG 2743
QY 972 GTTACTGAAGAAGCTCCATTAATAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACATATT 1031
Db 2744 GTACAGAGAGGAGGCCACCCCTTGAAGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATC 2803
QY 1032 GATGAAAAAGGGTACCGAGGCGCGCGCTATGTTCTCTGGAAGCTATTTCCCAATGAGCATT 1091
Db 2804 GACGAGAAAGGAGCTGAAGCTGTCTGGGCCCATGTTTTTAGAGGCCATACCCCATGTCTATC 2863
QY 1092 CCACCAGAAAGTTAAATTTAATAAACCAATTCGTTTTCTCTGATGATCGAGCAGAACACTAAA 1151
Db 2864 CCCCCCGAGGTCAAGTTTCAACAAACCCCTTTGCTTCTTTAATGATTGAACAAATATCCNAG 2923
QY 1152 AGCCCATTTGTTATGGGTAAAGTTGTCAACCCCAACTCAGAA 1192
Db 2924 TCTCCCTCTTTCATGGGAAAAAGTGTGAATCCCAACCCCAAAA 2964
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